From:	Steadman, David (AU1652)
Sent:	Wednesday, March 20, 2002 12:42 PM
To:	STIC-Biotech/ChemLib
Subject:	09/529,043 sequence search

NAME: David Steadman
AU: 1652
Date:03/20/02
Office: 10D-04
Mailbox: 10C-01 M3
Case Serial #: 09/529,043

Please search the following sequences for interference:

1) SEQ ID NO:2 (polypeptide sequence) against **polynucleotide** databases. = us-09-529-043b-2.flp

2) Nucleotides 165-3587 of SEQ ID NO:1 (polynucleotide sequence) against **polynucleotide** databases. = us-09-529-043b-1_copy_165_3587.flp

Please align the following sequences:

3) SEQ ID NO:1 of 09/529,043 against SEQ ID NO:1 of 09/220,081. = us-09-529-043b-1.res

4) SEQ ID NO:2 of 09/529,043 against SEQ ID NO:1 of 09/220,081. = us-09-529-043b-2.res

Please save search results to diskette.

Thank you very much,
David J. Steadman
308-3934
CM1, 10D-04

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher: _____ Bob	NA Sequences:_____	STN: _____
Phone: _____	AA Sequences:_____	DIALOG: _____
Location: _____	Structures:_____	Questel/Orbit: _____
Date Picked Up: 3-25-02	Bibliographic: _____	DRLink:_____
Date Completed: 3-26-02	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: _____	Full text:_____	Sequence Sys.: _____
Clerical: _____	Patent Family:_____	WWW/Internet: _____
Online time: _____	Other:_____	Other (specify): _____

EP9806210_1 1_$$_165_3587.Dna
Empro:Cgpyc

```
ID     CGPYC         standard; DNA; PRO; 3728 BP.
AC     Y09548;
NI     e1250842
DT     11-FEB-1998 (Rel. 54, Created)
DT     08-MAY-1998 (Rel. 55, Last updated, Version 2)
DE     Corynebacterium glutamicum pyc gene
KW     pyc gene; pyruvate carboxylase.
OS     Corynebacterium glutamicum
OC     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales;
OC     Corynebacterineae; Corynebacteriaceae; Corynebacterium.
RN     [1]
RA     Peters-Wendisch P.G., Kreutzer C., Kalinowski J., Patek M., Sahm H.,
RA     Eikmanns B.J.;
RT     "Pyruvate carboxylase from Corynebacterium glutamicum: characterization,
RT     expression and inactivation of the pyc gene";
RL     Microbiology 144:915-927(1998).
RN     [2]
RP     1-3728
RA     Peters-Wendisch P.G.;
RT     ;
RL     Submitted (21-NOV-1996) to the EMBL/GenBank/DDBJ databases.
RL     P.G. Peters-Wendisch, Institut fuer Biotechnologie 1, Forschungszentrum
RL     Juelich GmbH, Juelich, D-52425, FRG
DR     SPTREMBL; O54587; O54587.
FH     Key             Location/Qualifiers
FH
FT     source          1. .3728
FT                     /organism="Corynebacterium glutamicum"
FT                     /strain="ATCC 13032"
FT     CDS             165. .3587
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FT                     /db_xref="SPTREMBL:O54587"
FT                     /EC_number="6.4.1.1"
FT                     /product="pyruvate carboxylase"
FT                     /gene="pyc"
FT                     /translation="MSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYPRE
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FT     ECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTY
FT     PIFVKAVAGGGGRGMRFVASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQ
FT     ILGDHTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGA
FT     GTVEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDK
FT     IKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSML
FT     VKMTCRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHP
FT     HLLQAPPADDEQGRILDYLADVTVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRLK
FT     QLGPAAFARDLREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVE
FT     AWGGATYDVAMRFLFEDPWDRLDELREAMPNVNIQMLLRGRNTVGYTPYPDSVCRAFVK
FT     EAASSGVDIFRIFDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDY
FT     YLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTALRREFDLPVHVHTHDTAGGQLAT
FT     YFAAAQAGADAVDGASAPLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAV
     RGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQATALGLADRFELIEDNYAAVNEMLG
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SCORES   Initl: 17115 Initn: 17115 Opt: 17115 z-score: 25599.6 E():   0
100.0% identity in 3423 bp overlap

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              40        50        60        70        80        90
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                  160        170        180        190        200        210
EP9806210_1  CACCGCTCTTTTGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGCTCACCAGTCAAGGCG
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                  220        230        240        250        260        270
EP9806210_1  TACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTAC
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Cgpyc        TACCTGGACATCGATGAAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTTAC
                  380        390        400        410        420        430


                  280        290        300        310        320        330
EP9806210_1  CCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGC
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Cgpyc        CCGGGATACGGCTTCCTGTCTGAAAATGCCCAGCTTGCCCGCGAGTGTGCGGAAAACGGC
                  440        450        460        470        480        490


                  340        350        360        370        380        390
EP9806210_1  ATTACTTTTATTGGCCCAACCCCAGAGGTTCTTGATCTCACCGGTGATAAGTCTCGCGCG
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EP9806210_1  GTAACCGCCGCGAAGAAGGCTGGTCTGCCAGTTTTGGCGGAATCCACCCCGAGCAAAAAC
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                  460        470        480        490        500        510
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Cgpyc        ATCGATGAGATCGTTAAAAGCGCTGAAGGCCAGACTTACCCCATCTTTGTGAAGGCAGTT
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EP9806210_1  GCCGGTGGTGGCGGACGCGGTATGCGTTTTGTTGCTTCACCTGATGAGCTTCGCAAATTA
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EP9806210_1  GCAACAGAAGCATCTCGTGAAGCTGAAGCGGCTTTCGGCGATGGCGCGGTATATGTCGAA
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EP9806210_1  CGTGCTGTGATTAACCCTCAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAA
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                  760        770        780        790        800        810
EP9806210_1  ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA
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Cgpyc        ATTGCGCCAGCACAGCATTTGGATCCAGAACTGCGTGATCGCATTTGTGCGGATGCAGTA
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                820       830       840       850       860       870
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EP9806210_1  AAGGGCAACCACGTCTTCATCGAAATGAACCCACGTATCCAGGTTGAGCACACCGTGACT
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EP9806210_1  GAAGAAGTCACCGAGGTGGACCTGGTGAAGGCGCAGATGCGCTTGGCTGCTGGTGCAACC
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                1000      1010      1020      1030      1040      1050
EP9806210_1  TTGAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACGGTGCAGCACTGCAGTGC
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EP9806210_1  TACCGCTCACCAGGCGGAGCTGGCGTTCGTCTTGACGGTGCAGCTCAGCTCGGTGGCGAA
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                1240      1250      1260      1270      1280      1290
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                1300      1310      1320      1330      1340      1350
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                1360      1370      1380      1390      1400      1410
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Cgpyc        GGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAACAAGCCTCATGGTGTGCGTCCA
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EP9806210_1  AAGGATGTTGCAGCTCCTATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGC
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                   1780      1790      1800      1810      1820      1830
EP9806210_1  TTTGAGGATCCGTGGGACAGGCTCGACGAGCTGCGCGAGGCGATGCCGAATGTAAACATT
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                   1900      1910      1920      1930      1940      1950
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Cgpyc        CGCGCGTTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCCGCATCTTCGACGCG
                   2060      2070      2080      2090      2100      2110


                   1960      1970      1980      1990      2000      2010
EP9806210_1  CTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCG
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Cgpyc        CTTAACGACGTCTCCCAGATGCGTCCAGCAATCGACGCAGTCCTGGAGACCAACACCGCG
                   2120      2130      2140      2150      2160      2170


                   2020      2030      2040      2050      2060      2070
EP9806210_1  GTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTAC
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Cgpyc        GTAGCCGAGGTGGCTATGGCTTATTCTGGTGATCTCTCTGATCCAAATGAAAAGCTCTAC
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                   2080      2090      2100      2110      2120      2130
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                   2240      2250      2260      2270      2280      2290


                   2140      2150      2160      2170      2180      2190
EP9806210_1  GCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCA
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Cgpyc        GCCATTAAGGATATGGCTGGTCTGCTTCGCCCAGCTGCGGTAACCAAGCTGGTCACCGCA
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                   2200      2210      2220      2230      2240      2250
EP9806210_1  CTGCGCCGTGAATTCGATCTGCCAGTGCACGTGCACACCCACGACACTGCGGGTGGCCAG
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              2260      2270      2280      2290      2300      2310
EP9806210_1   CTGGCAACCTACTTTGCTGCAGCTGAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCA
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Cgpyc         CTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGCTTCCGCA
              2420      2430      2440      2450      2460      2470


              2320      2330      2340      2350      2360      2370
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              2480      2490      2500      2510      2520      2530


              2380      2390      2400      2410      2420      2430
EP9806210_1   ACCCGTCGCGATACCGGTTTGAGCCTCGAGGCTGTTTCTGACCTCGAGCCGTACTGGGAA
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              2440      2450      2460      2470      2480      2490
EP9806210_1   GCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTC
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Cgpyc         GCAGTGCGCGGACTGTACCTGCCATTTGAGTCTGGAACCCCAGGCCCAACCGGTCGCGTC
              2600      2610      2620      2630      2640      2650


              2500      2510      2520      2530      2540      2550
EP9806210_1   TACCGCCACGAAATCCCAGGCGGACAGTTGTCCAACCTGCGTGCACAGGCCACCGCACTG
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              2660      2670      2680      2690      2700      2710


              2560      2570      2580      2590      2600      2610
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              2620      2630      2640      2650      2660      2670
EP9806210_1   GGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTC
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Cgpyc         GGACGCCCAACCAAGGTCACCCCATCCTCCAAGGTTGTTGGCGACCTCGCACTCCACCTC
              2780      2790      2800      2810      2820      2830


              2680      2690      2700      2710      2720      2730
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              2840      2850      2860      2870      2880      2890


              2740      2750      2760      2770      2780      2790
EP9806210_1   GACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAG
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Cgpyc         GACTCTGTCATCGCGTTCCTGCGCGGCGAGCTTGGTAACCCTCCAGGTGGCTGGCCAGAG
              2900      2910      2920      2930      2940      2950


              2800      2810      2820      2830      2840      2850
EP9806210_1   CCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTT
              |||||||||||||||||||||||| :|:|||||||||||||||||||||||||||||||||
Cgpyc         CCACTGCGCACCCGCGCACTGGAAGGCCGCTCCGAAGGCAAGGCACCTCTGACGGAAGTT
              2960      2970      2980      2990      3000      3010


              2860      2870      2880      2890      2900      2910
EP9806210_1   CCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTC
              ||||||||||||||||||||||| :|:||||||||||||||||||||||||||||||||||
Cgpyc         CCTGAGGAAGAGCAGGCGCACCTCGACGCTGATGATTCCAAGGAACGTCGCAATAGCCTC
              3020      3030      3040      3050      3060      3070


              2920      2930      2940      2950      2960      2970
EP9806210_1   AACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGC
              |||||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||
Cgpyc         AACCGCCTGCTGTTCCCGAAGCCAACCGAAGAGTTCCTCGAGCACCGTCGCCGCTTCGGC
              3080      3090      3100      3110      3120      3130
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                 2980        2990       3000       3010       3020       3030
EP9806210_1  AACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        AACACCTCTGCGCTGGATGATCGTGAATTCTTCTACGGCCTGGTCGAAGGCCGCGAGACT
                 3140        3150       3160       3170       3180       3190


                 3040        3050       3060       3070       3080       3090
EP9806210_1  TTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        TTGATCCGCCTGCCAGATGTGCGCACCCCACTGCTTGTTCGCCTGGATGCGATCTCTGAG
                 3200        3210       3220       3230       3240       3250


                 3100        3110       3120       3130       3140       3150
EP9806210_1  CCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        CCAGACGATAAGGGTATGCGCAATGTTGTGGCCAACGTCAACGGCCAGATCCGCCCAATG
                 3260        3270       3280       3290       3300       3310


                 3160        3170       3180       3190       3200       3210
EP9806210_1  CGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        CGTGTGCGTGACCGCTCCGTTGAGTCTGTCACCGCAACCGCAGAAAAGGCAGATTCCTCC
                 3320        3330       3340       3350       3360       3370


                 3220        3230       3240       3250       3260       3270
EP9806210_1  AACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        AACAAGGGCCATGTTGCTGCACCATTCGCTGGTGTTGTCACCGTGACTGTTGCTGAAGGT
                 3380        3390       3400       3410       3420       3430


                 3280        3290       3300       3310       3320       3330
EP9806210_1  GATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        GATGAGGTCAAGGCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAGCAACA
                 3440        3450       3460       3470       3480       3490


                 3340        3350       3360       3370       3380       3390
EP9806210_1  ATCACTGCTTCTGTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Cgpyc        ATCACTGCTTCTGTTGACGGCAAAATCGATCGCGTTGTGGTTCCTGCTGCAACGAAGGTG
                 3500        3510       3520       3530       3540       3550


                 3400        3410       3420
EP9806210_1  GAAGGTGGCGACTTGATCGTCGTCGTTTCCTAA
             |||||||||||||||||||||||||||||||||
Cgpyc        GAAGGTGGCGACTTGATCGTCGTCGTTTCCTAAACCTTTCTGTAAAAAGCCCCGCGTCTT
                 3560        3570       3580       3590       3600       3610


Cgpyc        CCTCATGGAGGAGGCGGGGCTTTTTGGGCCAAGATGGGAGATGGGTGAGTTGGATTTGGT
                 3620        3630       3640       3650       3660       3670
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